

Genetic evaluation of an index of birth weight and yearling weight to improve efficiency of beef production^{1,2}

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ABSTRACT: The CGC population is a stabilized composite of ½ Red Angus, ¼ Charolais, and ¼ Tarentaise germplasm. The objectives of this research were to estimate genetic parameters for weight traits of CGC and to evaluate genetic responses resulting from selection based on the following index: $I = 365\text{-d weight} - 3.2(\text{birth weight})$. Phenotypes evaluated were birth weight ($n = 5,083$), 200-d weight ($n = 4,902$), 365-d weight ($n = 4,626$), and the index. In addition, there were 1,433 cows with at least one recorded weight, and 4,375 total observations of cow weight collected at the time their calves were weaned. In 1989, a randomly selected control line and a line selected for greater values of the index were established. Average generation intervals were 3.16 ± 0.04 and 3.90 ± 0.08 yr in the index and control lines, respectively. The index selection line ($n = 950$) accumulated approximately 212 kg more selection differential than the control line over three generations ($n = 912$). Heritability estimates for direct effects were 0.32 ± 0.04 , 0.49 ± 0.05 , 0.49 ± 0.05 , 0.30 ± 0.04 ,

and 0.70 ± 0.04 for the index, birth weight, 365-d weight, 200-d weight, and cow weight, respectively. Heritability estimates for maternal effects were 0.05 ± 0.02 , 0.11 ± 0.03 , 0.04 ± 0.02 , and 0.19 ± 0.04 for the index, birth weight, 365-d weight, and 200-d weight, respectively. In the control line, direct genetic changes for the index and its components were small. For the index selection line, direct genetic changes for the index, birth weight, 365-d weight, 200-d weight, and cow weight were 6.0 ± 0.3 , 0.45 ± 0.09 , 7.74 ± 0.55 , 3.42 ± 0.25 , and 6.3 ± 0.9 kg/generation, respectively. Maternal genetic changes were generally small for both the control and index selection lines. Thus, selection for the index produced positive correlated responses for direct genetic effects on BW traits at all ages, with only minor effects on maternal genetic effects. Results demonstrate that despite a genetic antagonism that compromises selection response for decreased birth weight and increased post-natal growth, favorable genetic responses can be achieved with the selection index used in this study.

Key Words: Beef Cattle, Genetic Gain, Selection Index, Selection Responses

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Introduction

Genetic improvement in efficiency of production has been a long-standing concern of beef cattle breeders

(e.g., Cartwright, 1970; Dickerson, 1976). Dickerson et al. (1974) proposed the index, $I = \text{yearling weight} - 3.2(\text{birth weight})$, as a criterion for selection to increase the economic efficiency of beef production. This index was predicted to increase economic efficiency of beef production by 6% relative to selection for yearling weight alone. Benefits of selection based on the index would result from reducing increases in: 1) mature cow size and thus feed inputs; and 2) calf birth weight and thus dystocia and associated mortality relative to selection on yearling weight. Increases in calf weights at weaning and yearling would be compromised by only approximately 10%.

Whereas estimates of genetic parameters for components of the index and weights at other ages are relatively commonplace, experimental evaluation of predicted selection responses is lacking. Thus, the primary objective of this research was to evaluate responses to genetic selection based on the index. Genetic parameters for the index, its components, and other growth traits were estimated in the course of this evaluation.

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Materials and Methods

This research made use of a composite population of beef cattle (CGC) developed by the USDA-ARS at Fort Keogh Livestock and Range Research Laboratory, Miles City, MT (Newman et al., 1993a,b). The general intent in forming the composite was to develop a strain of beef cattle with improved adaptation to the Northern Great Plains rangeland environment and with greater potential profitability than existing breeds. The CGC population was initiated by mating Charolais ($n = 14$) and Tarentaise ($n = 12$) sires to Red Angus dams ($n = 300$). The foundation matings were made from 1979 to 1983. Subsequently (1981 to 1987), F_1 bulls were mated to F_1 females to produce progeny that were $\frac{1}{2}$ Red Angus, $\frac{1}{4}$ Charolais, and $\frac{1}{4}$ Tarentaise. Animals of this breed composition were inter se mated in all subsequent generations. Generation numbers were calculated following the approach of Brinks et al. (1961). The straightbred Red Angus, Charolais, and Tarentaise used in founding the CGC population made up Generation 0. Generation numbers for descendants from Generation 0 were calculated as the average generation number of their parents plus one. Thus, direct breed effects were stabilized in Generation 2 and maternal breed effects were stabilized in the Generation 3. No additional germplasm has been introduced into CGC since the foundation matings. Additional details concerning the formation of the CGC population can be found in Newman et al. (1993a).

At Fort Keogh Livestock and Range Research Laboratory, annual precipitation averages 34 cm, with 21 cm received during March to July. Average temperatures range from -9°C in January to 23°C in July. The terrain is broken badlands and plains rangelands typical of the Northern Great Plains of the United States. Vegetation is predominantly western wheatgrass, blue gramma grass, buffalo grass, needle-and-thread, green needle grass, annual brome grasses, threadleaf sedge, greasewood, silver sagebrush, and fringe sagewort. Stocking rate is approximately one cow per 14 ha, with supplemental feed required during winter.

A 45-d breeding season began on approximately June 15 of each year. Cows were exposed for breeding in single-sire pastures until approximately August 1. In 1989 and 1990, yearling heifers and bulls were sent to the U.S. Sheep Experiment Station (Dubois, ID) for a mixed-species grazing trial. Mating occurred during the trial and all animals were returned to Miles City in late August of those years. After the breeding season, cows were grouped into two herds and grazed on native range until vegetation was covered by snow. Cows were weighed and pregnancy tested when their calves were weaned in early October. Nonpregnant females were culled. In preparation for calving, cows were moved to small pastures and fed approximately 9 kg of alfalfa hay per cow daily. As calving approached, first-calf heifers were observed periodically throughout each day. Older cows were observed only during daylight hours.

Calves were born primarily during late March, April, and early May. Male calves were not castrated and creep feed was not available to the calves. Calves were weaned at an average age of approximately 180 d. After weaning, calves were moved to a feedlot for a 140-d evaluation of postweaning growth. Before the test period began, the calves were allowed a pretest adjustment period of 2 to 4 wk following weaning. Bull calves were fed a ration that was formulated to support an average growth rate of 1.4 kg/d. The energy density of the ration was approximately 2.7 Mcal/kg. Crude protein content was approximately 12%. Primary ingredients in the ration were corn silage, barley, and a protein and mineral supplement. Heifer calves were fed to gain 0.8 kg/d. The approximate energy density and CP content of the diet were 2.4 Mcal/kg and 9%, respectively. Calves were weighed twice at the beginning and at the end of the postweaning test period. Birth weight and gain from birth to weaning were adjusted for differences in age of dam following the results of Newman et al. (1993b). Multiplicative adjustment factors for birth weight were 1.088, 1.040, and 1.036 for calves with 2-, 3-, and 4-yr-old dams, respectively. Multiplicative adjustment factors for gain from birth to weaning were 1.197, 1.105, and 1.043 for calves with 2-, 3-, and 4-yr-old dams, respectively. Weights of calves from 5-yr-old and older cows were not adjusted. Weaning and yearling weights were adjusted to 200-d and 365-d age-constant bases using the procedures recommended by the BIF (1996).

In 1988, the population was divided at random into three lines. Bulls for the first line were selected based on the following index: $I = 365\text{-d weight} - 3.2(\text{birth weight})$ (Dickerson et al., 1974). Bulls for the second line were selected based on the ratio of their adjusted weaning weight to the coincident mature equivalent weight of their dam. Results from selection on the ratio are discussed in a subsequent paper. Selection decisions were based on phenotypic performance within year. Virtually all selection pressure was applied to males and most females were exposed for breeding as yearlings. Bulls for the third line were selected at random. All bulls were required to pass a breeding soundness examination as yearlings before being used for breeding. Within line, matings were planned to avoid inbreeding of the progeny produced in the next generation, subject to the constraint that approximately equal numbers of females of similar ages were assigned to each sire.

In 1988 and 1989, the process of stabilizing the genetic composition of CGC was ongoing, and only those bulls and cows from Generation 3 or greater contributed to the selection experiment. Hence, numbers of cows and calves in the control and index selection lines were less than their numbers in subsequent years. Numbers of calves born each year are shown in Table 1. Cows were culled from both the index and control lines when they were not diagnosed pregnant in the fall when their calf was weaned. When necessary to maintain the inventory of cows at approximately 120 per line, older

Table 1. Numbers of calves (n), generation numbers (G_n), and cumulative selection differentials for birth weight, 365-d weight, and the index reflecting selection applied, by year of birth and line.

Year	Index line								Control line							
	n	G_n	Birth weight, kg		365-d weight, kg		Index, kg		n	G_n	Birth weight, kg		365-d weight, kg		Index, kg	
			Sire	Dam	Sire	Dam	Sire	Dam			Sire	Dam	Sire	Dam	Sire	Dam
1989	25	4.0	13.8	3.6	190	52	151	43	28	4.0	6.5	-6.2	89	49	74	71
1990	49	4.3	1.6	0.8	208	45	204	45	51	4.1	4.2	-1.8	37	50	24	58
1991	79	4.0	-11.3	-0.5	150	26	190	30	85	4.2	2.4	-0.1	8	52	3	55
1992	97	4.2	-1.1	1.3	244	64	251	63	95	4.3	5.9	-0.9	85	37	68	42
1993	103	4.7	7.2	-1.5	227	76	207	84	96	4.8	8.7	0.2	61	38	36	40
1994	94	5.0	-4.7	-1.9	310	108	329	118	92	5.1	9.4	-1.4	166	34	139	42
1995	83	5.3	0.0	0.5	287	124	291	126	97	5.4	-2.4	2.6	84	47	98	43
1996	81	5.8	-3.0	0.4	314	162	330	164	56	5.8	5.8	2.0	91	66	77	64
1997	85	6.0	-4.7	0.7	296	179	316	181	57	6.1	3.1	2.3	67	59	60	56
1998	88	6.5	-3.6	0.0	328	153	343	158	57	6.3	3.3	3.9	63	66	56	59
1999	100	6.5	-5.1	0.2	328	192	362	198	115	6.2	3.1	3.6	59	65	52	58
2000	66	7.1	-5.4	1.3	382	212	404	217	83	6.4	3.2	2.4	69	70	62	67

cows were removed from the experiment regardless of their phenotype or progeny performance. In 1995 to 1997, a sample of cows was also removed from the experiment to initiate a project for mapping quantitative trait loci (MacNeil and Grosz, 2002). Within line, these cows were removed randomly; however, more cows were taken from the control line than from the index-selected line. In general, the experimental design was to use four yearling bulls as sires in each line during each breeding season with one of those sires, selected at random, to be used the next year as a 2-yr-old. In the index selection line, exceptions to the planned design occurred in the 1990 breeding season when nine yearling bulls were used, and in 1996 to 1999 when five yearling bulls were used each year. In the control line, exceptions to the planned design occurred in the 1990 breeding season when nine yearling bulls were used; the 1996 to 1998 breeding seasons when the same six bulls were used; and the 1999 breeding season when four of the six bulls used in 1998 were used again and the other two bulls used in 1998 were replaced by sons. Increasing the number of bulls used per year while reducing the number of cows allowed the effective population size of the control line to remain approximately equal to that of the index selection line during the latter years of this research.

Individual selection differentials (**ID**) were computed for the index and component traits within year-sex-line subclasses based on the adjusted phenotypes. Cumulative selection differentials were calculated following the methodology of Newman et al. (1973) as modified by Koch et al. (1994) to assess differences in selection applied between sires and dams. Total cumulative selection = $ID + (CS + CD)/2$, with $CS = [\text{sum of (sire IDs)} + \text{sum of (SCS + DCS)}/2]/n$ and $CD = [\text{sum of (dam IDs)} + \text{sum of (SCD + DCD)}/2]/n$. In these formulas, CS = cumulative sire differential, CD = cumulative dam differential, SCS = sire's cumulative sire differential, DCS = dam's cumulative sire differential, SCD = sire's cumulative dam differential, DCD = dam's cumulative dam

differential, and n = number in a contemporary group. Performance records were not available for the purchased females and their contemporaries or for the purebred bulls used by AI and their contemporaries. Therefore, in calculating the cumulative selection differentials, the deviation of an individual's phenotype from the contemporary group mean was assumed to be zero for all animals born before 1980.

Genetic parameters were estimated from phenotypes recorded from all animals born between 1980 and 2000. Pedigree information was extended to the founding purebreds, which were assumed to be unrelated. Results from preliminary ANOVA indicated that year of birth, sex of calf, age of dam, and a variety of two-factor interactions among these traits affected the index and its components. Hence, contemporary groups for the birth, 200-d, and 365-d weights and the index were formed as year, sex, and age of dam subclasses for further analyses. Derivative-free multiple-trait REML (Smith and Graser, 1986; Graser et al., 1987) methods, as implemented by Boldman et al. (1995), were used to predict breeding values upon convergence of estimates of the (co)variance components. Linear models for birth weight ($n = 5,083$), 200-d weight ($n = 4,902$), 365-d weight ($n = 4,626$), and the index ($n = 4,626$) were similar and included fixed contemporary groups and random direct and maternal additive effects and uncorrelated random maternal permanent environmental effects of the dams. Cows ranged in age from 2 to 11 yr, with an average age of 3.6 yr. For cow weight, contemporary groups were formed as year-age subclasses with cows older than five years coded as being five years of age. There were 1,433 cows with at least one recorded weight and a total of 4,375 observations. The linear model for cow weight included fixed contemporary group effects, random direct additive effects, and uncorrelated random permanent environmental effects associated with repeated records of the cow. Multiple trait analyses, constructed using the models described above, allowed for correlations among the additive ef-

fects, among the uncorrelated random effects, and among residual errors. Genetic trends for the index and control lines were estimated from the regression of predicted breeding values on generation numbers of animals born in the respective lines between 1989 and 2000. Standard errors of these regression coefficients are underestimated due to correlations among breeding values arising from repeated use of cows and bulls and also from drift. Results from three sets of analyses are reported here: 1) a single-trait analysis of the index; 2) four two-trait analyses of the index with birth weight, 200-d weight, 365-d weight, and cow weight; and 3) three two-trait analyses of 365-d weight with birth weight, 200-d weight, and cow weight. Results from the multiple trait analyses were used to discern correlated responses to selection and predict the magnitude of responses due to selection based on the index relative to responses that would be expected from selection based on 365-d weight. The multiple-trait derivative-free maximum likelihood method used here involves maximizing the likelihood function (Λ), given the data and is equivalent to minimizing $-2 \log \Lambda$. Each analysis was assumed to have converged when the variance of $-2 \log \Lambda$ in the simplex was less than 10^{-10} and the scaled parameter estimates changed by less than 0.01 in a reanalysis of the data using updated starting values.

Following Dodenhoff et al. (1988), standard errors of the estimated variance components and scaled parameter estimates were calculated from the inverse of the negative average information matrix considering it to be an asymptotic dispersion matrix of the estimated parameters. Parameter estimates were derived from all recorded phenotypes, as described above. However, to make calculating the average information matrix feasible in multiple-trait analyses, only those records with all the phenotypes measured were used in calculating the standard errors.

Results and Discussion

Generation numbers (Table 1) reflect the elapsed generations since the original foundation of CGC with the purebred Red Angus, Charolais, and Tarentaise designated as Generation 0. The average generation interval for the index line was 3.16 ± 0.04 yr. The average generation interval for the control line was 3.90 ± 0.08 yr. The difference in average generation interval was the result of use of the same control line bulls for more than 1 yr beginning in 1996.

Selection differentials for calves born in the early years of this experiment reflect the accumulated selection applied in the process of stabilizing the breed composition of CGC. Thus, initial differences in selection differentials between the index and control lines primarily reflect the differences in individual deviations of the selected sires (Table 1). At the termination of the experiment (i.e., 1999 and 2000), selection differential for the index was approximately 212 kg greater for the

index selection line than for the control line. The trend across years in the cumulative selection differentials for birth weight in the index line was not significant. Cumulative selection differentials for both yearling weight and the index increased markedly across years in the index line. In the control line, trends across years were significantly positive for the maternal cumulative selection differentials for birth weight and yearling weight, but not for the index. These trends in the control line were the result of small heifers failing to breed and/or to calve successfully which resulted in their being culled. Similar factors influenced the maternal cumulative selection differentials in the index selection line.

With the single-trait analysis, estimates for direct and maternal heritability of the index were 0.32 ± 0.04 and 0.05 ± 0.02 , respectively. The estimated genetic correlation between direct and maternal additive effects was -0.18 ± 0.13 . Maternal permanent environmental effects and residual effects accounted for 0.09 ± 0.02 and 0.56 ± 0.03 of the phenotypic variance, respectively. Comparable parameter estimates for the index were not found in the literature, but can be derived from the numerous reports of parameter estimates for birth and 365-d weights found in the literature.

Genetic trends in the index are presented in Figure 1 for both lines. These trends result from the selection applied and drift, which are inseparable in experiments without replicated lines, and from sampling error (Falconer, 1989). Regressions of direct and maternal breeding values on generation number indicated no genetic change for the control line. For the index selection line, direct genetic change was 6.0 ± 0.3 kg per generation, and the maternal genetic trend was 0.3 ± 0.6 kg per generation. Total response based on estimates of genetic change was materially less than would be predicted from the heritability estimates and intensity selection applied.

Birth weight and 365-d weight, the components of the index, were analyzed jointly to further dissect response to selection. Heritability estimates for direct effects on birth weight and 365-d weight were 0.49 ± 0.05 and 0.49 ± 0.05 . The existence of a genetic antagonism, which limits the potential for reducing birth weight and increasing growth to a year of age, was supported by the estimate of the genetic correlation (0.71 ± 0.05) between direct effects on birth and 365-d weight. Heritability estimates for maternal effects for birth weight and 365-d weight were 0.11 ± 0.03 and 0.04 ± 0.02 , which were much smaller than the corresponding estimates for the direct effects. The present heritability estimates for direct effects are slightly greater and estimates for maternal effects slightly less than the average of estimates summarized by Koots et al. (1994). As with the genetic correlation between direct effects, the estimate of the correlation between maternal genetic effects was positive (0.51 ± 0.17). Estimates of genetic correlations between direct and maternal effects across traits were generally small and not

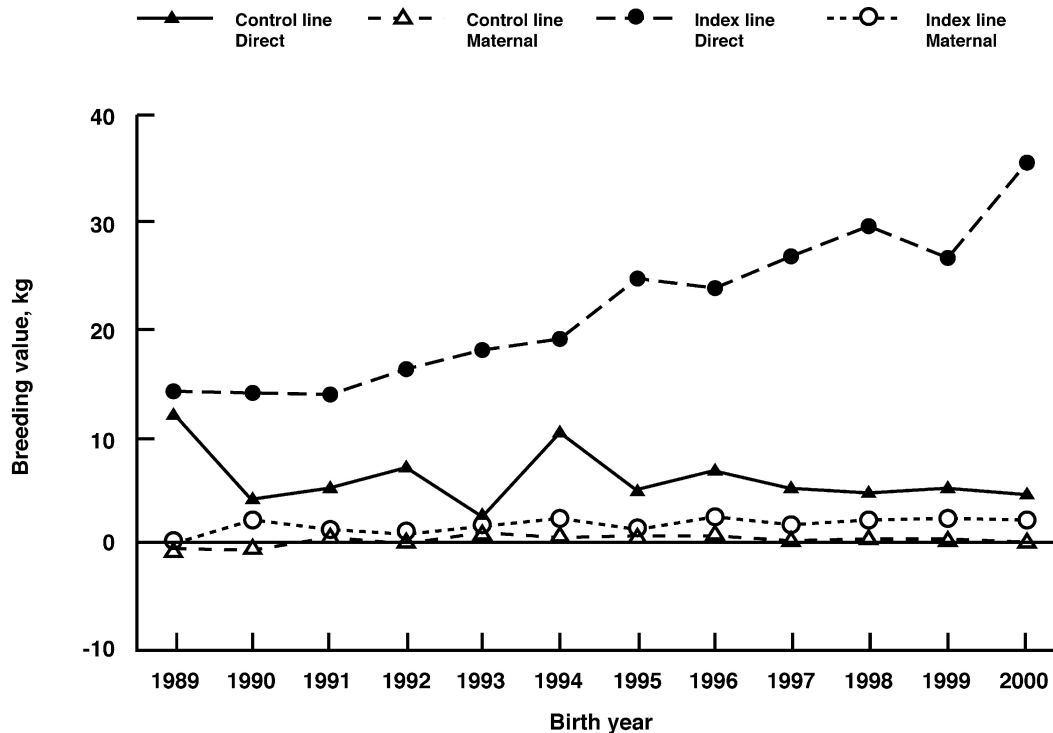


Figure 1. Trends in direct and maternal breeding values for the index for the control and index selection lines.

significant. Permanent environmental effects due to dams accounted for essentially none of the variance in birth weight and 0.07 ± 0.02 of the variance in 365-d weight.

Figures 2 and 3 show estimates of genetic trend in birth weight and 365-d weight for the control line and in response to selection on the index, 365-d weight – 3.2(birth weight), respectively. Whereas the direct and

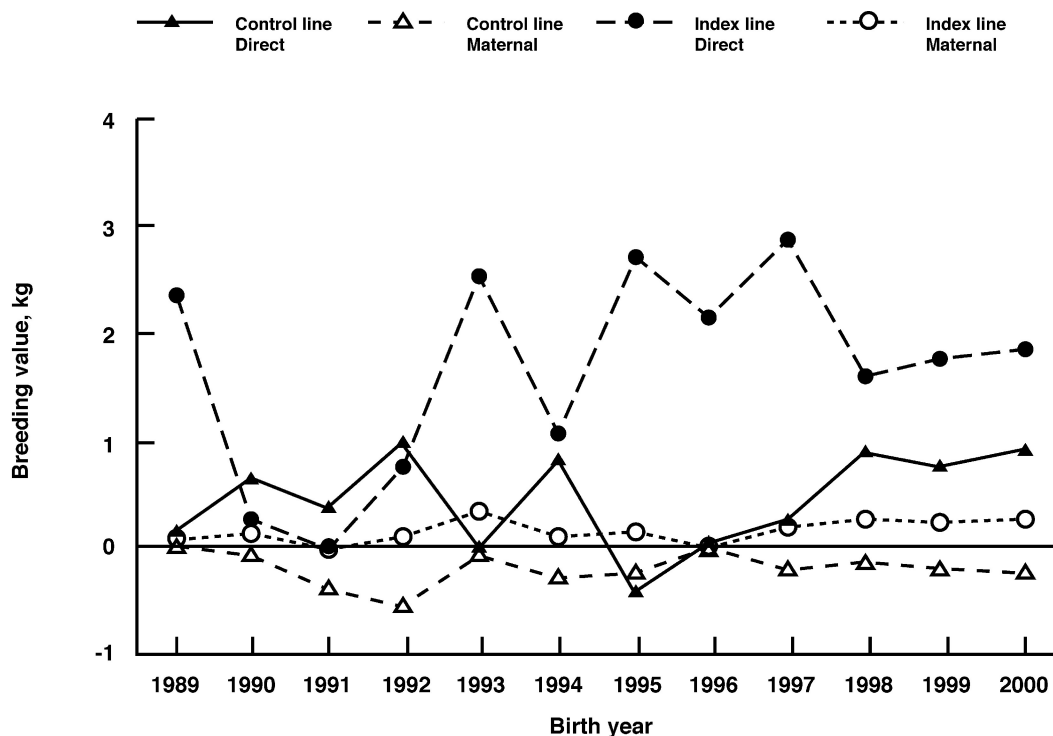


Figure 2. Trends in direct and maternal breeding values for birth weight for the control and index selection lines.

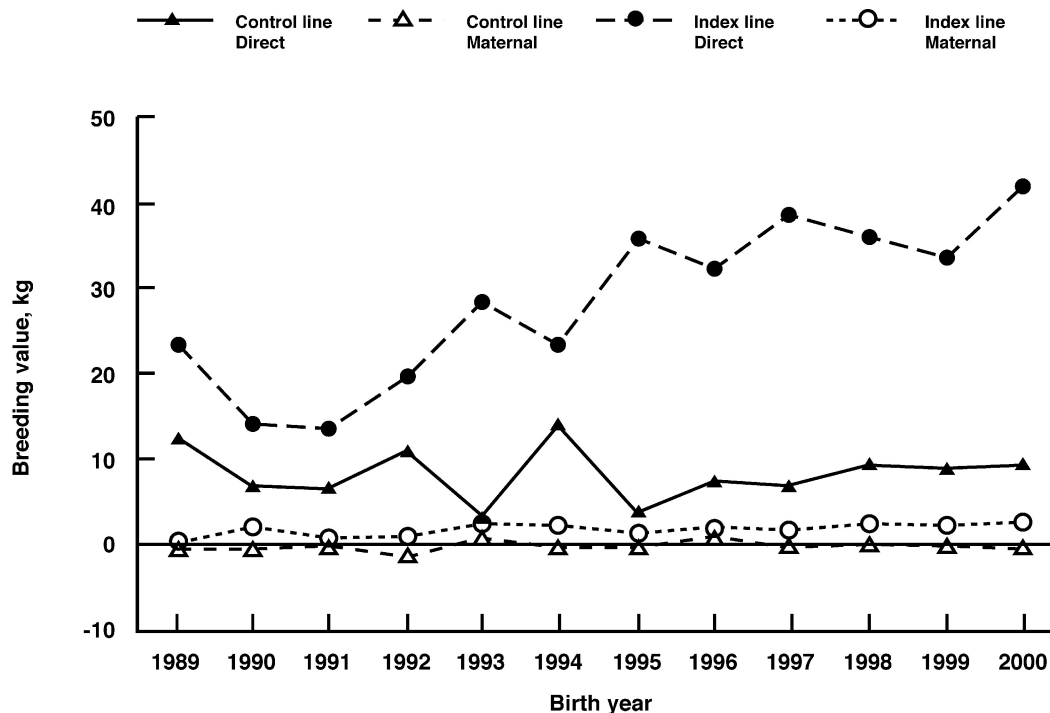


Figure 3. Trends in direct and maternal breeding values for 365-d weight for the control and index selection lines.

maternal trends for birth weight and 365-d weight observed in the control line were significantly different from zero, they were quite small. For the control line, regressions of breeding values on generation number were 0.18 ± 0.08 , 0.08 ± 0.03 , 1.70 ± 0.65 , and 0.25 ± 0.10 per generation for direct and maternal effects for birth and 365-d weights, respectively. Corresponding estimates of genetic change for the index selected line were 0.45 ± 0.09 , 0.04 ± 0.02 , 7.74 ± 0.55 , and 0.39 ± 0.08 per generation.

In formulating the selection index used in this experiment, Dickerson et al. (1974) explicitly considered only direct genetic effects for birth weight and yearling weight. The heritability estimates used in developing the selection index were similar to those for the direct effects found in the present research. Given the small estimates of heritability for maternal effect and the apparent lack of important correlations between direct and maternal effects found in this study, we would anticipate responses similar to those predicted by Dickerson et al. (1974). The primary difference between parameters estimated from these data and those used earlier in developing the selection index is the substantially stronger genetic antagonism between direct effects on birth weight and 365-d weight found in these data (i.e., 0.46 vs. 0.71).

Dickerson et al. (1974) predicted selection on the index yearling weight $-3.2(\text{birth weight})$ would substantially reduce, but not eliminate, the increase in birth weight. Although a comparable positive control (i.e., a line selected for increased yearling weight alone) was not used in the present study, the response in birth

weight was small and a substantial genetic increase was observed for 365-d weight.

MacNeil et al. (1998) eliminated the direct genetic increase in birth weight by selecting for below-average birth weight and maximal yearling weight using independent culling levels while maintaining positive, albeit slower (36%), genetic increase in yearling weight. Index in retrospect calculations (our unpublished results) show the emphasis placed on birth weight by this independent culling levels strategy was not significantly different from -3.2 employed in this experiment. However, the genetic increase in direct genetic effects on 365-d weight found here is essentially twice that observed in the line selected using independent culling levels by MacNeil et al. (1998). A partial explanation for this difference in genetic change may be the greater heritabilities for all traits in the CGC composite than in the Line 1 Hereford population and the greater efficiency of index selection relative to independent culling levels.

Consistent with average estimates from the literature (Koots et al., 1994), direct and maternal effects on 200-d weight were moderately heritable in these data; 0.30 ± 0.04 and 0.19 ± 0.04 , respectively. The genetic correlation between direct and maternal effects was 0.08 ± 0.11 . Permanent environmental effects due to dams accounted for 0.10 ± 0.02 of the phenotypic variation in 200-d weight. As would be expected from the part-whole relationship between 200-d weight and the index, correlations between direct effects, maternal effects, permanent environment effects, and temporary environment effects influencing the two traits were all

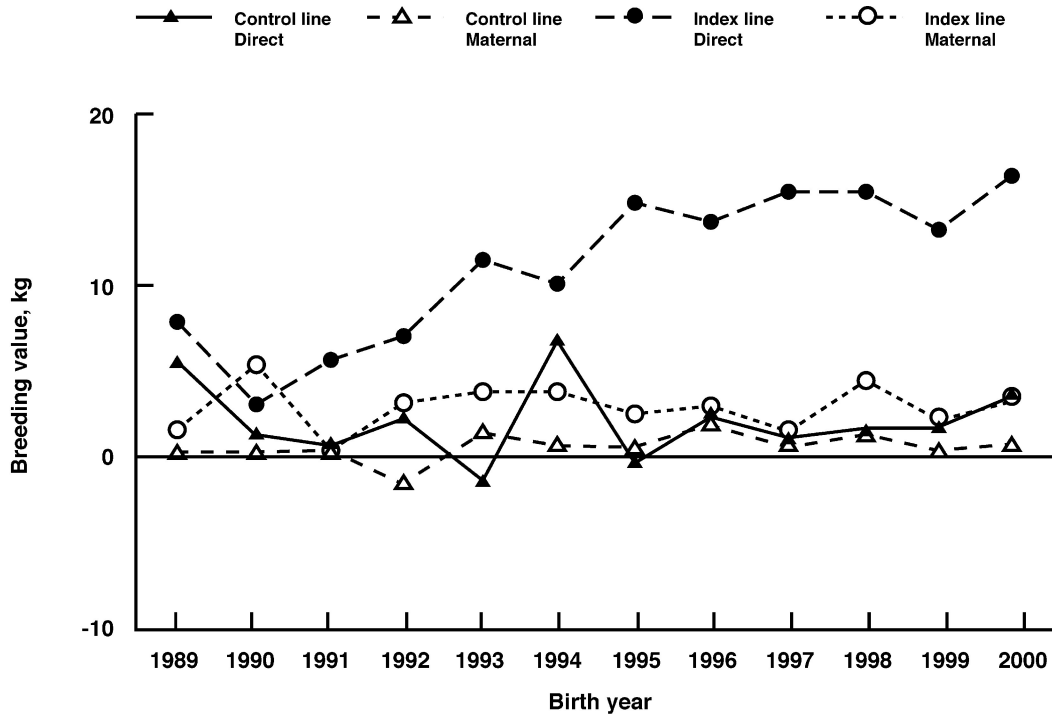


Figure 4. Trends in direct and maternal breeding values for 200-d weight for the control and index selection lines.

large; 0.70 ± 0.05 , 0.93 ± 0.06 , 0.93 ± 0.07 , and 0.64 ± 0.02 , respectively. Genetic changes in direct and maternal effects due to the correlated response in 200-d weight are shown in Figure 4. For the control line, regressions of breeding values for 200-d weight on generation number were 0.84 ± 0.30 and 0.60 ± 0.18 for direct and maternal effects for 200-d weight. Corresponding estimates of genetic changes in the index selected line were 3.42 ± 0.25 and 0.31 ± 0.16 per generation.

Cow weight was highly heritable (0.70 ± 0.04), which is somewhat greater than the average of estimates from the literature summarized by Koots et al. (1994). Correlations of direct genetic effects on cow weight with direct and maternal genetic effects on the index were 0.77 ± 0.06 and -0.07 ± 0.04 , respectively. The permanent environmental correlation among repeated weight records was 0.13 ± 0.03 . Thus, repeatability of cow weight was 0.82. Trends in direct breeding values for cow weight are shown in Figure 5. Regressions of direct breeding values for cow weight on generation number were -5.0 ± 1.2 and 6.3 ± 0.9 for the control and index lines, respectively. Given the small positive genetic trends for weights at young ages in the control line, there appears to have been some natural selection against greater cow weight in this environment. However, the genetic trend for cow weight in the index selection line remained positive, but of slightly less magnitude than direct response for 365-d weight (7.4 kg), suggesting that no further increase in body weight accrued at subsequent ages for 365-d weight of cows.

Taken together, selection for the index $I = 365\text{-d weight} - 3.2(\text{birth weight})$ proposed by Dickerson et al.

(1974) produced positive correlated responses for direct genetic effects for body weight traits at all ages and only minor responses for maternal genetic effects. Considering only the direct effects and using the estimated genetic parameters, the relative correlated responses for birth, 200-d, 365-d, and cow weights due to selection for the index versus selection for yearling weight were predicted. Based on these data, predicted genetic responses for birth weight, 200-d weight, 365-d weight, and cow weight to selection for the index would be 13, 67, 73, and 68% of those resulting from selection for 365-d weight. The index appeared to be more effective in controlling the rate of increase in birth weight than was predicted by Dickerson et al. (1974). However, the sacrifices in the correlated responses of 200- and 365-d weight were also somewhat greater than predicted earlier by Dickerson et al. (1974). In the case of 200-d weight, both the lower heritability of the index relative to the heritability of 365-d weight (0.32 vs. 0.49) and from the lower genetic correlation between 200-d weight and the index relative to the genetic correlation between 200-d weight and 365-d weight (0.70 vs. 0.85) contribute to this effect. As the genetic correlation between 365-d weight and the index is very high (0.90), the difference in heritability between 365-d weight and the index accounts most of the predicted reduction in response of 365-d weight. The increase in cow size that is anticipated to result from selection to increase growth to 1 yr of age was also moderated by selection for the index in the present experiment. Certainly, the substantially greater genetic correlation between cow weight and 365-d weight derived from these data than

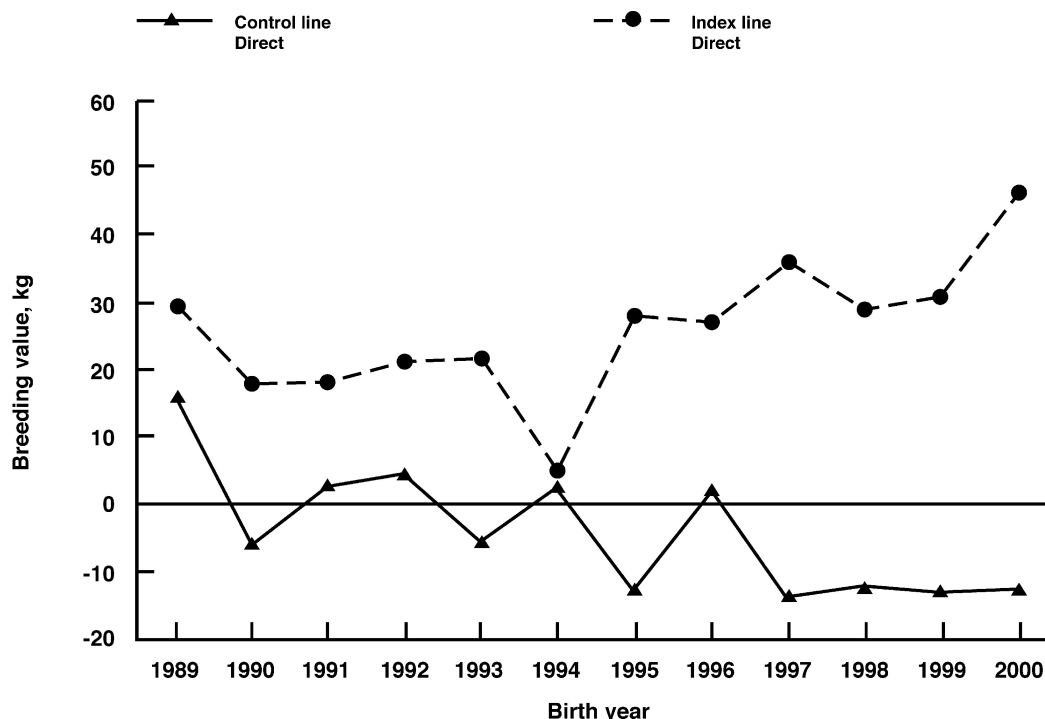


Figure 5. Trends in direct breeding values for cow weight for the control and index selection lines.

the value used by Dickerson et al. (1974) (0.92 vs. 0.64) contributes to this result.

When interpreting the present results, it should be remembered that this experiment was approximately three generations in duration. Since selection was primarily of sires and because maternal responses lag the responses for direct effects by a generation, any conclusion that this selection strategy only impacts the direct effects would be premature. In addition, the index selection line and the control line were not replicated and the results may be affected by drift.

Implications

Results demonstrate that despite a genetic antagonism that compromises selection response for decreased birth weight and increased postnatal growth, significant favorable genetic responses can be achieved with the selection index used in this study. Selection for the index had a favorable effect on the shape of the growth curve, restricting response in birth weight and mature weight of cows. Selection intensity in this experimental setting would be decreased relative to that which would be available across a breed using national cattle evaluation and AI. Thus, to the extent that selection against birth weight and for greater subsequent growth increases efficiency of beef production, seedstock producers have even greater potential to make progress than can be demonstrated in a research setting.

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